



hDEC2a

DEC1

MDEGIPHLQERQ—L——LEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDQTYKLPHRLIEKKRRDRIN 61  
M-ERIPSAQPPPACLPKAPGLEHGDLPGMYPAHMYQVYKSRRGIKRSEDSKETYKLPHRLIEKKRRDRIN 69

ECIAQLKOLLPEHLKLTTLGHLEKAVLETLKHLKALTALTEQQHQKIIALQNG---ERSLKSPIQSD 127  
ECIAQLKDLLPEHLKLTTLGHLEKAVLETLKHVKALTNLIDQQQQKIIALQSGLQAGELSGR-NVETG 138

LDAFHSGFOTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGA---PS 194  
QEMFCSGFOTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAPKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAELAAENDTDTDGYGGEAEARPD-R-E---K- 254  
SPAKGSEG-P---G-K---N---CVPVIQRTFAHSSGEQSGSDTDGYGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAAALLGPDPAAAALLR 317  
DHGRRFTMGERIGAIKQESE-E-PPTKKNRMQLSDDEGHFTSS—————D————— 305

PDAALLSSLVAFGGGGAPFP-QPAAAAPFCLPFCFLSP-SAAAAYQPFLDKSGLEKYLYPAAAAPF 385  
—LISS—PFLG—PHPHQP—PFCLPF-YLIPPSATA-YL-PML—EKCWYPTSV—P— 349

PLLPGIPAPAAAAAAAAAAFPCLSSVLSPPPEKAGAAATLL-PHEVAPLGAPHQPHGRTH 454.  
VL-YPGLNASAAA—————LSSFMNP—DKISA—PLLMPQR—L—PSP————— 385

LPFAGPREPGNPESSA—QE—DPSQPGK—EA—P 482  
LP-AHP—SVDSVLLQALKPIPPLNLETKD

(Homology 43%)

FIG. 1



hDEC2a

hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKR00TK--DTYKLPHRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKR00TKVSDTYKLPHRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQS0LDAFHSGFQTC 138

DLLPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQS0LDAFHSGFQTC 140

AKEVLQYLSRFESWTPREPCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

QKLEPLAYCVPVIQRTQPSAELAAENDTDTSGYGGEEARPDREKGKGAGASRVTIKQEPPGEDSPARK 278

QKLEPLAYCVPVIQRTQPSAELAAENDTDTSGYGGEEARPDREKGKGAGASRVTIKQEPPGEDSPARK 280

RMKLDSRGGSGGGPGGGAAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAPFC 348

RMKLDSRGGSGGGPGGGAAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAPFC 350

LPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLPGIPAPAAAAAAAAAFPCLSSV 418

LPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLPGIPAPAAAAAAAAAFPCLSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 484

FIG. 2

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hDEC2a

mDEC2a

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDCKDTYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSOLDAFHSGFQTCAK 140

LPEHLKLTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTSGYGGEAEPDREKGKGAGASRVTIKQEPPGEDS-P 275

SGP--ERVARCVPVIQRTQPGTEP--EHDTDTDSGYGGEAE-QG-R----A-A--V--KQEPPG-DSSP 249

APKRMKLDRGGGGGGGGGGGAAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGGAPFPQPAAAAA 345

APKRKPKEARG-----ALLGPEPA---LL---G---SLVAL---GGGAPFAQPAAA--- 288

PFCLPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAFPCL 415

PFCLPFYLLSPSAA-YVQPWLDKSGLDKYLYPAAA-PFPLLYPGIPA-----AAAAAAAAAFPCL 348

SSVLSPPPKEKAGA-AAATLLPHEVAPLGAP-HPQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

SSVLSPPPKEKAGATAGAPFLAHEVAPPG-PLRPQAHSRTHLPRAV-----NPESS-QEDATQPAKDAP 410

FIG. 3



hDEC2a

mDEC2a

SHARP-1

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70  
MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDOTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70  
MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDOTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIALQNGERSLKSPIQSDDLDAFHSGFQTCAK 140  
LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIALQNGERSLKSPPVQADLDAFHSGFQTCAK 140  
LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIALQNGERSLKSPPVQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQVPLSK-GTG-AP-SAAGSAAAPCLERA 207  
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196  
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCPVVIQRTQPSAELAAENDTDGDSGYGGEAEARPDREKGKGAGASRVTIKQEPPGEDS-P 275  
SGP-ERVARCPVVIQRTQPGTEP-EHDTDGDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DSSP 249  
SGS-ERVARCPVVIQRTQPGTEP-EHDTDGDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DPSL 249

APKRMKLDRGGSGGPGGGAAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAA 345  
APKRPKLEARG-----ALLGPEPA---LL---G---SLVAL---GGGAPFAQPAAA--- 288  
RPRG 253

PFCLPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLPGIPAPAAAAAAAAAAAFPCL 415  
PFCLPFYLLSPSAAA-YVQPWLDSGLDKYLYPAAA-PFPLLPGIPA-----AAAAAAAFAFPC 348

SSVLSPPEKAGA-AAATLLPHEVAPLGAP-HPQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482  
SSVLSPPEKAGATAGAPFLAHEVAPPG-PLRPQHHSRTHLPRAV-----NPESS-QEDATQPAKDAP 410

FIG. 4